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Research Article

Two new species and a new host record of Hyphomycetes associated with decaying wood in Yunnan Province, China

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Abstract

In recent years, there has been certain progress in the research on fungal diversity in Yunnan Province, China, particularly in aquatic habitats. This study introduces two new species, *Ellisembia yuxiense* and *Sporidesmium ailaoshanense*, as well as a new host record of *Sporidesmium tropicale* on *Pinus yunnanensis* from freshwater habitats in Yunnan Province. All taxa were identified by integrating morphological traits with phylogenetic analysis of combined LSU, ITS, and *rpb*2 DNA sequences. Comprehensive morpho-anatomical descriptions and detailed illustrations are provided to elucidate the characteristics of each taxon.

Key words: 2 new taxa, asexual morph, phylogeny, Sporidesmiales, taxonomy

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Introduction

The family Sporidesmiaceae was initially erected by Fries (1849) but remained neglected mainly until the availability of molecular data and re-examination of its type genus, *Sporidesmium*. Su et al. (2016) resurrected Sporidesmiaceae to accommodate specific taxa with available molecular data and morphological characteristics similar to *Sporidesmium ehrenbergii*, the lectotype species of *Sporidesmium*. Members of this family are typically saprobic or mycoparasitic, commonly found inhabiting decaying wood and plant debris in both terrestrial and freshwater ecosystems (Su et al. 2016). *Sporidesmium* was the sole genus in the family until Subramanian

(1992) segregated *Ellisembia* to accommodate species characterized by distoseptate conidia (pseudosepta) and proliferating conidiophores.

However, given the lack of phylogenetic support for the taxonomic significance of euseptate and distoseptate conidia among *sporidesmium*-like species, Su et al. (2016) proposed that *Ellisembia* should be considered a synonym of *Sporidesmium* sensu stricto. However, Delgado et al. (2024) reevaluated the group using fresh collections of the type species *Ellisembia coronata* from its German type locality and rejected the synonymy of *Ellisembia* under *Sporidesmium*. Their multigene analyses revealed that *Ellisembia coronata* forms a distinct monophyletic lineage within Sporidesmiaceae, clearly separated from *Sporidesmium*. By restricting *Ellisembia* to this lineage—characterized by distoseptate conidia and conidiophores with few or no percurrent extensions—the authors realigned the genus with the original concept from Subramanian (1992). Currently, Species Fungorum lists 69 species under *Ellisembia* and 186 species under *Sporidesmium* (accessed 24 July 2025).

Our recent studies on aquatic fungi from Southwestern China have revealed several novel taxa and new records, including two novel species (*Memnoniella chrysanthemi* and *Craspedodidymum hunanense*) and a new record (*Aquadictyospora clematidis*) (Liu et al. 2024; Habib et al. 2025). In this study, we introduce two new species within the Sporidesmiaceae—*Ellisembia yuxiense* and *Sporidesmium ailaoshanense*—and report a new host record for another *Sporidesmium* species. Through phylogenetic analysis, we confirm the placement of these new species within their respective generic clades, while detailed morphological comparisons distinguish them from similar taxa.

Materials and methods

Sample collection

Between August and October 2024, researchers collected specimens of decaying branches and logs submerged in streams and lakes from Ailaoshan National Nature Reserve and Wumengshan National Nature Reserve in Yunnan Province, China. These specimens were packed in sealed plastic bags, and collection in formation was recorded (Rathnayaka et al. 2024); they were then transported to the mycology laboratory at Guizhou Medical University. The specimens were examined in the laboratory. Specimens that did not produce spores were placed in a sealed storage container and subjected to humidified incubation at 24 °C. Sterile water was sprayed into the container daily to maintain humidity levels, and the specimens were observed for spore production. All specimens were deposited at the herbarium of Guizhou Medical University (GMBH) and the Herbarium of Cryptogams, Herbarium of Kunming Institute of Botany, Chinese Academy of Sciences (KUN-HKAS).

Morphological characterization and isolation

Macroscopic characteristics were examined under an Olympus SZ61 stereomicroscope (Japan) and photographed with a Canon 700D digital camera (Canon, Tokyo, Japan). Samples were mounted in water for microscopic observation. Quantitative measurements focused on internal structures, including the diameter, height,

color, and shape of the conidiomata. The length and width of conidiophores and conidia were precisely measured, with width consistently recorded at the broadest point to ensure accuracy and comparability. The Tarosoft® Image Frame Work (v0.9.7) program and Adobe Photoshop CS6 software (Adobe Systems, USA) were used for measuring and processing images. Single-spore isolation was performed following the method described by Liu et al. (2024). A small volume of sterile water was used to suspend the conidia, which were then thoroughly mixed and evenly spread onto water agar (WA) plates. After 10 to 24 hours of incubation, germinated conidia were examined using a stereomicroscope and transferred to potato dextrose agar (PDA) plates. All cultures were incubated at 24 °C.

DNA extraction, polymerase chain reaction (PCR) amplification, and sequencing

Colonies were cultivated on potato dextrose agar (PDA) plates for 2 to 4 weeks until the hyphae fully colonized the medium or growth ceased. Fresh mycelia were then gently scraped using a sterile scalpel for DNA extraction. Total genomic DNA was isolated using the BIOMIGA Fungal Genomic DNA Extraction Kit (TAKARA RR047A, China), following the manufacturer's instructions. PCR amplification targeted three regions: the internal transcribed spacer (ITS), the large subunit rDNA (LSU), and a partial fragment of the second-largest subunit of RNA polymerase II (*rpb2*). Primer pairs used were ITS5/ITS4 for ITS (White et al. 1990), LR0R/LR5 for LSU (White et al. 1990), and fRPB2-5f/fRPB2-7cR for *rpb2* (Liu et al. 1999; Sung et al. 2007; Voglmayr et al. 2016). PCR reactions were performed in a 25 μL mixture containing 9.5 μL of double-distilled water, 12.5 μL of PCR Master Mix, 1 μL of each primer, and 1 μL of template DNA. PCR products were verified by 1.5% agarose gel electrophoresis, stained with GoldenView, and sent to Sangon Biotech (China) for sequencing.

Phylogenetic analyses

The reference sequences retrieved from open databases originated from recently published data and BLASTn results of closely matching sequences. Sequences were aligned using the MAFFT v.7.110 online program (Katoh et al. 2019) with default settings. The alignments were adjusted manually using BioEdit v.7.0.5.3 (Hall 1999) where necessary. Maximum likelihood (ML) analyses were performed using RAxML v.8.2.12 with the GTRGAMMA substitution model and 1,000 bootstrap replicates (Stamatakis 2014). Phylogenetic analyses were also performed for Bayesian inference in MrBayes v.3.2.2 (Ronquist et al. 2012) online. Markov chain Monte Carlo (MCMC) sampling in MrBayes v.3.2.2 (Ronquist et al. 2012) was used to determine posterior probabilities (PP). Six simultaneous Markov chains were run for 1,000,000 generations, and trees were sampled every 1,000th generation. The first 25% of the trees were discarded as burn-ins. The remainder was used to calculate the posterior probabilities (PPs) for individual branches. The phylogenetic tree was visualized in FIGTREE v.1.4.3 (Rambaut 2012). All analyses were conducted on the CIPRES Science Gateway v3.3 web portal (Miller et al. 2010). All obtained sequences were deposited in GenBank (Table 1). The outgroups and loci used in phylogenetic analyses, tailored to specific families and genera—including ITS, LSU, and

Table 1. Taxa and corresponding GenBank accession numbers of sequences used in the phylogenetic analysis.

Name	Strain	Type	GenBank accession numbers			References
			ITS	LSU	*rpb2*	
Ellisembia bambusicola	HKUCC 3578	–	–	DQ408562	–	Shenoy et al. 2006
Ellisembia calyptrata	HKUCC 10821	T	–	DQ408564	DQ435085	Tian et al. 2024
Ellisembia cryptomeriae	UESTCC 23.0227	T	OR887405	OR887115	PP076811	Tian et al. 2024
Ellisembia coronata	CCF 6699	–	OR886656	OR886656	–	Delgado et al. 2024
Ellisembia cangshanensis	MFLUCC 15-0420	–	–	KU376273	–	Su et al. 2016
Ellisembia minigelatinosa	NN 47497	–	–	DQ408567	–	Shenoy et al. 2006
Ellisembia pseudobambusae	CCF 6709	–	OR886657	OR886657	PP349741	Tian et al. 2024
Ellisembia sp.	HKUCC 10558	–	–	DQ408565	DQ435088	Shenoy et al. 2006
Ellisembia melaleucae	CPC 32707	T	MH327817	NG_064550	–	Tian et al. 2024
Ellisembia melaleucae	CPC 32936	–	MH327818	MH327854	–	Tian et al. 2024
Ellisembia spiraeae	CBS 148298	T	NR_175218	NG_081327	OK651164	Tian et al. 2024
Ellisembia spiraeae	CPC 39766	–	OK664716	OK663755	–	Tian et al. 2024
Ellisembia yuxiensis	GMB5104	T	PV779542	PV779549	PV78284	This study
Ellisembia yuxiensis	GMB5108	–	PV779546	PV779552	PV782985	This study
Sporidesmium ailaoshanensis	GMB5103	T	PV779542	PV779548	PV782982	This study
Sporidesmium ailaoshanensis	GMB5107	–	PV779545	PV779551	PV782983	This study
Sporidesmium appendiculatum	MFLU 18-0981	T	MW286500	MW287774	–	Dong et al. 2021
Sporidesmium aturbinatum	DLUCC 1417	–	MZ420743	MZ420758	MZ442697	Tian et al. 2024
Sporidesmium chiangmaiense	MFLUCC 18-0999	–	MW286497	MW287771	–	Dong et al. 2021
Sporidesmium dulongense	MFLUCC 17-0116	T	MH795812	MH795817	MH801190	Tian et al. 2024
Sporidesmium fluminicola	MFLUCC 15-0346	–	–	KU376271	–	Su et al. 2016
Sporidesmium lageniforme	MFLU 18-1594	T	MK828640	MK849782	MN124533	Tian et al. 2024
Sporidesmium lignicola	DLUCC 1376	–	–	MK849783	–	Yang et al. 2023
Sporidesmium lignicola	KUMCC 15-0266	T	–	MK849784	–	Yang et al. 2023
Sporidesmium luminicola	MFLUCC 15-0346	–	–	KU376271	–	Yang et al. 2023
Sporidesmium parvum	HKUCC 10836	–	–	DQ408558	–	Su et al. 2016
Sporidesmium pyriformatum	MFLUCC 15-0620	T	KX710146	KX710141	MF135649	Tian et al. 2024
Sporidesmium pyriformatum	MFLUCC 15-0627	–	KX710148	KX710143	MF135650	Tian et al. 2024
Sporidesmium submersum	MFLUCC 15-0421	T	–	KU376272	–	Su et al. 2016
Sporidesmium tetracoilum	CBS 126412	–	MH864106	MH875566	–	Vu et al. 2019
Sporidesmium tetracoilum	PRC 4681	–	OU413153	OU413153	–	Vu et al. 2019
Sporidesmium thailandense	MFLUCC 15-0964	T	–	MF374370	MF370955	Tian et al. 2024
Sporidesmium thailandense	MFLUCC 15-0617	–	–	MF077561	–	Delgado et al. 2024
Sporidesmium tropicale	MFLU 17–0850	–	MF077551	MF077562	MF135646	Yang et al. 2018
Sporidesmium tropicale	DLUCC:1689	–	MZ420745	MZ420760	MZ442698	Bao et al. 2021
Sporidesmium tropicale	MFLUCC 17-0344	–	OL780513	OL782088	–	Senwanna et al. 2021
Sporidesmium tropicale	GMB5105	–	PV779544	PV779550	PV782986	This study
Sporidesmium tropicale	GMB5109	–	PV779547	PV779553	PV782987	This study
Sporoschisma hemipsilum	CBS 414.61	–	MH858104	MH869677	–	Delgado et al. 2024
Sporoschisma hemipsilum	KUMCC 15-0227	–	KX455866	KX455859	–	Delgado et al. 2024
Sporoschisma hemipsilum	MFLUCC 17-1712	–	MK828616	MK835816	–	Delgado et al. 2024
Sporoschisma juvenile	MFLUCC 18-1348	–	MK828619	MK835819	–	Delgado et al. 2024
Tracylla aristata	CBS 141404	–	OL654129	OL654186	–	Tian et al. 2024
Tracylla aristata	CPC 25500	–	KX306770	KX306795	–	Tian et al. 2024

Notes: –: no data available; T: type specimens or strains.

rpb2—were chosen based on published literature. The best-scoring RAxML tree is presented in the phylogenetic figures, and the phylogenetic placement of isolated strains is detailed in the notes section of each respective taxon.

Results

Phylogenetic analyses

The concatenated ITS–LSU–*rpb2* alignment of the Sporidesmiaceae dataset consisted of 46 taxa, including the outgroups. *Tracylla aristata* CBS-141404 and *T. aristata* CPC-25500 (Réblová et al. 2021) were selected as the outgroup taxon. The combined aligned sequence matrix comprises ITS (632 bp), LSU (1,568 bp), and *rpb2* (1,150 bp) sequence data, totaling 3,450 characters. The tree topology derived from maximum likelihood (ML) analysis closely resembled that of Bayesian inference (BI) analysis. The best-scoring RAxML tree is shown in Fig. 1. The phylogenetic tree based on BI and ML approaches confirmed the position of our newly generated sequences nested within the phylogenetic branch of the genera *Ellisembia* and *Sporidesmium* (Fig. 1). Two of our isolates cluster within the *Sporidesmium* clade, one representing a novel species that appeared as a sister to *Sporidesmium dulongense* (MFLUCC 17-0116), albeit with low statistical support. However, this topology was recovered consistently across multiple analyses. The second *Sporidesmium* isolate groups with *Sporidesmium tropicale* with high support (ML/BI = 100/1). The isolate of *Ellisembia yuxiense* sp. nov. (GMB5104, GMB5108) formed a well-supported clade (ML/BI = 100/1) that is sister to a lineage containing *E. calyptrata* (HKUCC 10821) and *E. cryptomeriae* (UESTCC 23 0227).

Taxonomy

Ellisembia yuxiense **Q.F. Zhang, K. Habib & Q.R. Li, sp. nov.**
MycoBank No: 859647
Fig. 2

Etymology. The specific epithet refers to the location where the holotype specimen was collected, Yuxi City.

Type. CHINA • Yunnan Province, Yuxi City, Ailaoshan National Nature Reserve (24°5'7.01"N, 101°31'30.44"E), altitude: 1169 m, on moist decayed branch, 15 September 2024, Qinfang Zhang, 2024ALS177-1 (GMB5104, holotype; GMBC5104, ex-type); KUN-HKAS 146987, isotype.

Description. ***Saprobic*** on decaying twigs of an unknown branch. ***Sexual morph***: undetermined. ***Asexual morph***: ***Mycelium*** superficial, septate, light brown to brown, numerous, scattered, single or in groups. ***Conidiophores*** 81–158 × 4–6 µm (av. = 110.3 × 5.1 µm, *n* = 30), macronematous, mononematous, solitary or caespitose, erect, verruculose, straight or slightly curved, becoming slightly narrower towards the apex, 7–12-septate, smooth-walled, unbranched. ***Conidiogenous cells*** 3–6 × 2–4 µm (av. = 4.7 × 3.8 µm, *n* = 30), monoblastic, integrated, pale brown, terminal, cylindrical. ***Conidia*** 24–57 µm (av. = 40.4, *n* = 30) long, 6–9 µm (av. = 8.8 µm, *n* = 30) wide at the broadest part, tapering to 2–4 µm (av. = 3.4 µm, n = 30) wide at apex, 2–5 µm (av. = 3.4 µm, n = 30) wide at base, solitary, acrogenous, smooth, obclavate, truncate at the base, gray to light brown, without a mucilaginous cap, 5–9-distoseptate, and also 3–5 euseptate.

Culture characteristics. Conidia germinate on water agar within 12 hours. At 24 °C, colonies growing on PDA reach a diameter of 10–15 mm after 7 weeks. Colonies convex, surface rough, moist, uneven, from above grayish-white, reverse dark brown to black. No pigmentation was produced in the culture medium.

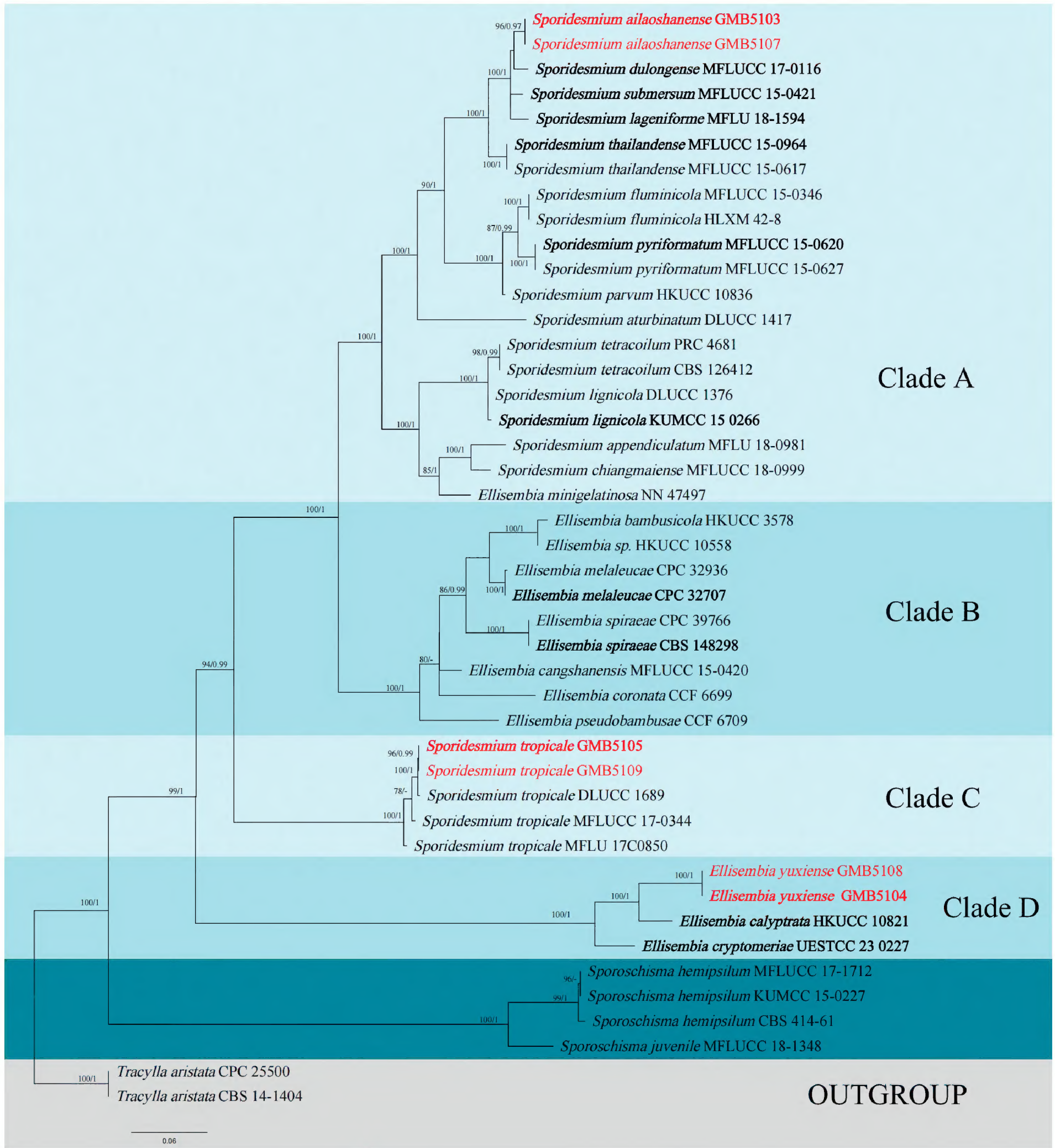

Figure 1. RAxML tree based on a combined ITS, LSU, and *rpb2* gene sequences data set. Bootstrap support values for maximum likelihood (ML) ≥ 75% and Bayesian posterior probabilities (BPP) ≥ 0.95 are displayed above or below the respective branches (ML/BI). New species and new host species are highlighted in red font, while type materials are displayed in bold black font.

Additional material examined. CHINA • Yunnan Province, Yuxi City, Ailaoshan National Nature Reserve (28°19'21.77"N, 104°00'19.21"E), altitude: 1419 m, on moist decayed branch, 15 September 2024, Qinfang Zhang, 2024ALS175 (GMB5108; GMBC5108).

Notes. Phylogenetically, *Ellisembia yuxiense* formed a well-supported sister branch to *E. calyptrata* (HKUCC-10821) (Fig. 1). However, the two species can be readily distinguished by conidiophore and conidia dimensions.

Figure 2. *Ellisembia yuxiense* (GMB5104, Holotype) **A.** Specimen; **B–D.** Conidiophores and conidia on natural substratum; **E.** Germinating conidium; **F, G.** Conidiophores and conidia; **H.** Conidiogenous cells and conidia; **I, J.** Conidia; **K, L.** Surface and reverse view of culture on PDA. Scale bars: 1 mm (**B**); 0.5 mm (**C**); 0.1 mm (**D**); 10 µm (**E–J**).

Table 2. Morphological comparison of Clade C (Fig. 1) and Ellisembia species.

Names	Strain	Conidiophores	Conidiogenous cells	Conidia	Reference
Ellisembia calyptrata	HKUCC 10821	verruculose. Brown to dark brown, 30–50 × 6.0–7.0 µm.	monoblastic, integrated, pale brown, terminal, cylindrical.	obclavate, truncate at the base, tapering to the apex, 6–17-septate, pale brown to dark brown, 60–90 × 9.0–12.0 µm.	Wu and Zhuang 2005
E. coronata	CCF 6699	(1–)2–5(–6)-septate, 0–2 ampulliform, lageniform or subcylindrical percurrent extensions, Brown to dark reddish brown, 18–66 × 5–7 µm.	monoblastic, integrated, pale brown, terminal, cylindrical	narrowly obclavate, less often subcylindrical or subfusiform, sometimes short rostrate, pale brown, smooth, 7–14-distoseptat, Brown to dark brown, (40–)52–89(–101) × 8–11 µm.	Delgado et al. 2024
E. cryptomeriae	UESTCC 23 0227	4–12-septate, verruculose. Brown to dark brown, 45–140 × 5–10 µm.	monoblastic, integrated, pale brown, terminal, cylindrical, 4–15 × 3–5 µm.	obclavate, truncate at the base, tapering to the apex, 6–17-septate, pale brown to dark brown, 20–85 × 7–14 µm.	Tian et al. 2024
E. melaleucae	CPC 32707	1-2-septate, erect, subcylindrical, dark brown, 12–30 × 4–6 µm.	terminal, medium brown, smooth, subcylindrical, holoblastic, 5–20 × 4–5 µm.	medium brown, smooth, obclavate, straight to flexuous, apexobtuse, base obconically truncate, 5-21-disto-septate, (45–)80–130(–170) × (8–)9–10(–11) µm.	Crous et al. 2018
E. spiraeae	CBS148298	1-4-septate, erect, dark brown, subcylindrical, unbranched, 15–40 × 5–7 µm.	terminal, integrated, subcylindrical, blastic, medium brown, smooth-walled, 10–20 × 5-–6 µm.	solitary, obclavate, straight to flexuous, apex subobtuse, base obconically truncate, (4-)6–10-distoseptate, (45–)70–85(–100) × (8–)9(–10) µm.	Crous et al. 2021
E. yuxiense	GMB5104, GMB5108	7–12-septate, verruculose. Brown to dark brown, 81–158 × 4–6 µm.	monoblastic, integrated, pale brown, terminal, cylindrical. 3–6 × 2–4 µm.	obclavate, truncate at the base, tapering to the apex, 5–9-septate, pale brown to dark brown. 24–57 × 6–9 µm.	This study

Ellisembia yuxiense has significantly longer conidiophores (81–158 × 4–6 µm) compared to *E. calyptrata* (30–50 × 6–7 µm) and smaller conidia (24–57 × 6–9 µm vs. 60–90 × 9–12 µm) (Wu and Zhuang 2005; Shenoy et al. 2006). Morphologically, *Ellisembia yuxiense* resembles *E. cryptomeriae* in conidiophore size; however, the latter can be distinguished by its larger conidia, 20–85 × 7–14 µm with 6–17 septa, compared to *E. yuxiense*, which has conidia 24–57 × 6–9 µm with 5–9 septa. Differences from other morphologically similar species are provided in Table 2.

Furthermore, only the LSU and *rpb*2 sequence data are accessible for *E. calyptrata*. A comparison of sequence data of the LSU and *rpb*2 between *E. yuxiense* (GMB5104) and *E. calyptrata* (HKUCC-10821) shows 98.57% sequence identity in LSU and 88.72% sequence identity in *rpb*2.

***Sporidesmium ailaoshanense* Q.F. Zhang & Q.R. Li, sp. nov.**

MycoBank No: 859648

Fig. 3

Etymology. The specific epithet refers to the location where the holotype specimen was collected, Ailaoshan National Nature Reserve.

Type. CHINA • Yunnan Province, Ailaoshan National Nature Reserve (24°5'7.01"N, 101°31'30.44"E), altitude: 1169 m, on dry rotten wood, 15

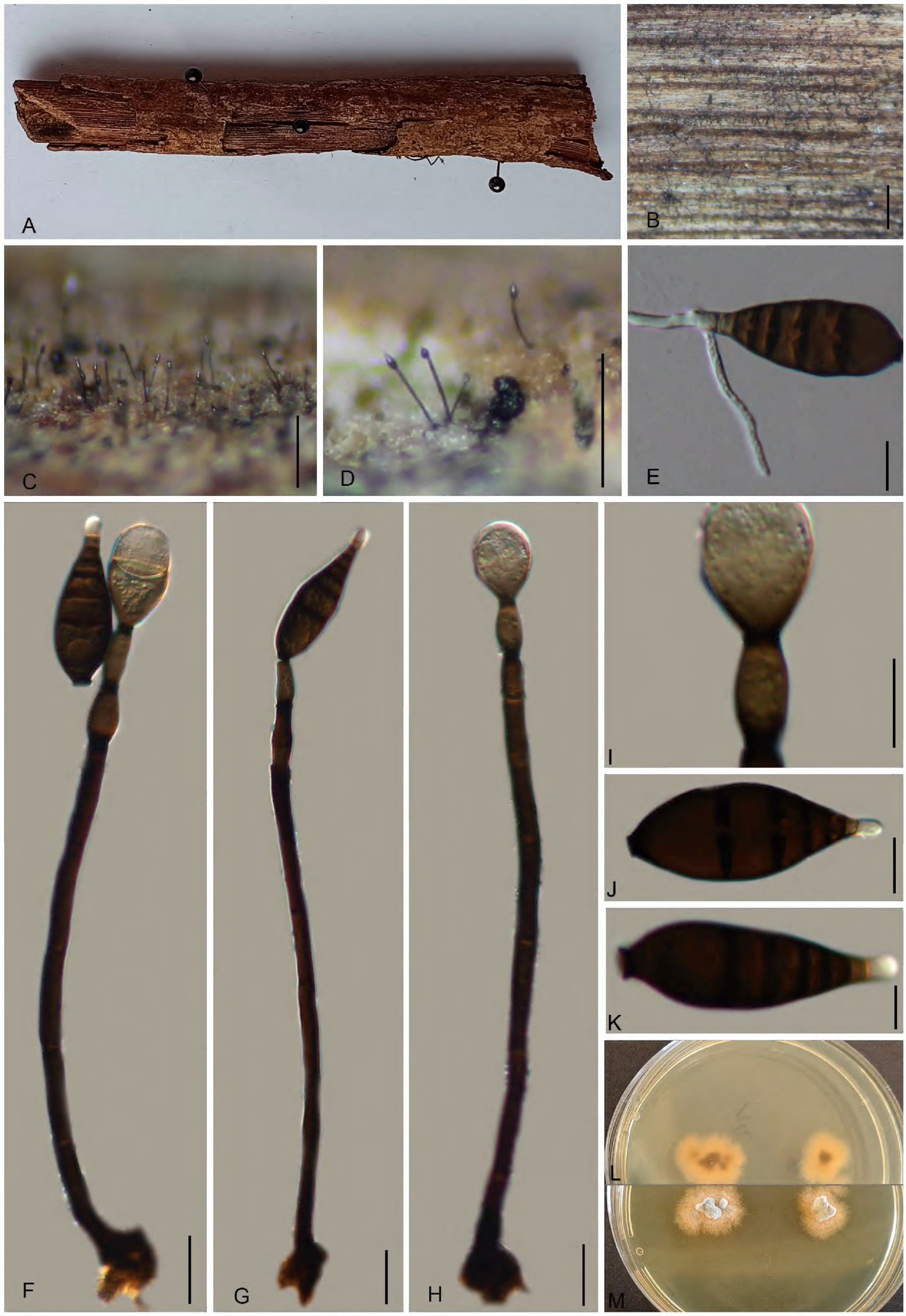

Figure 3. ***Sporidesmium ailaoshanense*** **(GMB5103, Holotype) A.** Specimen; **B–D.** Conidiophores and conidia on natural substratum; **E.** Germinating conidium; **F–H.** Conidiophores and conidia; **I.** Conidiogenous cell; **J, K.** Conidia; **L, M.** Surface and reverse view of culture on PDA. Scale bars: 1 mm (**B**); 0.25 mm (**C, D**); 10 µm (**E–K**).

September 2024, Qinfang Zhang, 2024ALS74 (GMB5103, holotype; GMBC5103, ex-type); KUN-HKAS 146988, isotype.

Description. ***Saprobic*** on decaying twigs of an unknown wood. ***Sexual morph*:** undetermined. ***Asexual morph*: *Colonies*** on the substratum superficial, effuse, scattered, hairy, black. ***Mycelium*** immersed, composed of branched, septate, smooth, pale brown to brown hyphae. ***Conidiophores*** 110–184 × 4–7 µm (av. = 135 × 6.2 µm, *n* = 30), macronematous, mononematous, unbranched, erect, straight or slightly flexuous, smooth, thick-walled, septate, not clear, cylindrical, dark brown, paler towards apex, smooth, and thick-walled. ***Conidiogenous cells*** 10–16 × 4–9 µm (av. = 13.2 × 7.1 µm, *n* = 30), monoblastic, integrated, determinate or sometimes percurrently proliferating, terminal, pale brown, cylindrical. ***Conidia*** 42–58 × 13–22 µm (av. = 49.0 × 17.4 µm, *n* = 30), acrogenous, solitary, dry, pyriform or lageniform, truncate at the base, smooth, dark brown, paler towards the apex, 4–5 µm wide and truncate at the base, thick-walled, 3–5 µm wide at the apex, 6–8-septate, slightly constricted at the septa, ***Conidial secession*** schizolytic.

Culture characteristics. Conidia germinate on WA within 12 hours. At 25 °C, colonies growing on PDA reach a diameter of 20–30 mm after three weeks. The colonies are convex, with a smooth surface, mycelium present, dry, flat, and wrinkle-free. From above, the center appears white, with a grayish-white edge, while from below, the colony center is dark brown to black. No pigmentation is produced in the culture medium.

Additional material examined. CHINA • Yunnan Province, Ailaoshan National Nature Reserve (24°5'4.82"N, 101°31'32.89"E), altitude: 1131 m, on a dry wood branch, 15 September 2024, Qinfang Zhang, 2024ALS131 (GMB5107, GMBC5107).

Notes. Phylogenetically, *Sporidesmium ailaoshanense* is closely related to *S. dulongense* (MFLUCC-17-0116) (Fig. 1). Morphologically, the two species share similar conidial shape and length. However, *S. ailaoshanense* can be distinguished by its longer conidiophores (110–184 µm vs. 88–124 µm) and wider conidia (13–22 µm vs. 13–15 µm) (Hyde et al. 2020). Moreover, *S. dulongense* has conidia with a long hyaline apex, which is very short in *S. ailaoshanense*. Base pair comparisons also support their separation; the ITS, LSU, and *rpb*2 sequences of *S. ailaoshanense* (GMB5103) and *S. dulongense* (MFLUCC-17-0116) show 97.0% sequence identity in ITS, 99.6% in LSU, and 97.64% in *rpb*2.

Sporidesmium submersum also shares a similar conidial shape and length with *S. ailaoshanense*, including a short hyaline apex. However, it differs in having much shorter conidiophores (59–72 µm vs. 110–184 µm) and thinner conidia (14–16 µm vs. 13–22 µm) (Su et al. 2016).

Sporidesmium tropicale **M.B. Ellis, Mycol. Pap. 70: 58 (1958)**
MycoBank No: 306326
Fig. 4

Host. *Pinus yunnanensis* Franch.

Description. ***Saprobic*** on submerged decaying branch of *Pinus yunnanensis*. ***Sexual morph*:** undetermined. ***Asexual morph*: *Colonies*** on superficial substratum, scattered, hairy, effuse, and black. ***Mycelium*** mostly immersed, composed of septate, branched, pale black, and smooth-walled hyphae. ***Conidiophores*** 76–392 × 4–8 µm (av. = 239 × 7.0 µm, *n* = 30), macronematous, mononematous,

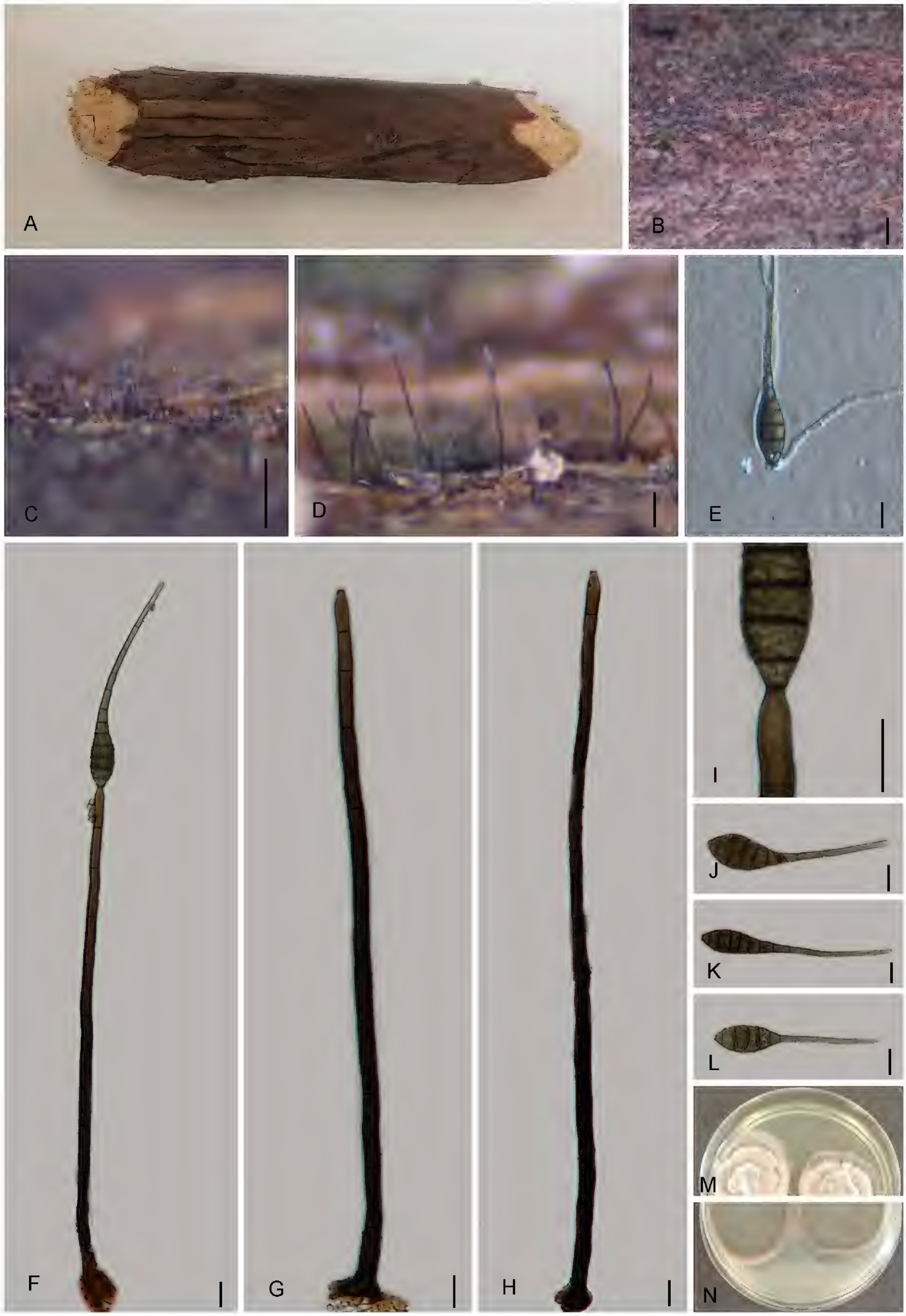

Figure 4. *Sporidesmium tropicale* (GMB5109) **A.** Specimen; **B–D.** Conidiophores and conidia on natural substratum; **E.** Germinating conidium; **F–H.** Conidiophores and Conidia; **I.** Conidiogenous cells; **J, M.** Conidia. Scale bars: 1 mm (**B**); 0.5 mm (**C, D**); 10 µm (**E–M**).

unbranched, cylindrical, erect, straight or slightly flexuous, single, 5–17-septate, dark brown, paler towards apex, smooth, and thick-walled. ***Conidiogenous cells*** 4–11 × 3–5 µm (av. = 6.1 × 4.0 µm, *n* = 30), monoblastic, holoblastic, terminal, integrated, cylindrical, and dark-brown. ***Conidia*** 65–134 × 12–16 µm (av. = 105 × 14.8 µm, *n* = 30), acrogenous, solitary, dry, pyriform, rostrate, obclavate, with a long and slender apex, straight or slightly curved, tapering to the apex, 3–5 µm wide and truncate at the base, dark brown, pale brown, 2–5 µm wide at the apex, 11–17-septate, thick-walled, and with the proximal part usually verrucose.

Material examined. CHINA • Yunnan Province, Wumengshan National Nature Reserve (28°19'29.79"N, 104°00'05.48"E), altitude: 1361 m, on *Pinus yunnanensis* Franch., decaying wood, 22 July 2024, Qinfang Zhang, 2024WMS80 (GMB5105). CHINA • Yunnan Province, Wumengshan National Nature Reserve (28°19'15.23"N, 104°0'16.31"E), altitude: 1373 m, on dry wood, 22 July 2024, Qinfang Zhang, 2024WMS96 (GMB5109).

Notes. In the phylogram (Fig. 1), our collections (*Sporidesmium tropicale* GMB5105 and GMB5109) clustered with *S. tropicale* (DLUCC-1689) with strong statistical support (ML/BY: 100/1). DNA sequence comparisons revealed high similarity to *S. tropicale* (DLUCC-1689), with 99.38% identity in the ITS, 100.00% in the LSU, and 99.71% in the *rpb*2 gene. However, noticeable morphological differences were observed when compared to both the original description by Ellis (1958) and the description provided by Bao et al. (2021), particularly in the size of the conidiophores and conidia.

The conidiophores in our collection (*S. tropicale* GMB5105) are longer (76–392 × 4–8 µm) than those reported by Bao et al. (2021) for *S. tropicale* (DLUCC-1689) (71–163 × 5–8 µm), while the conidia are slightly smaller (65–134 × 12–16 µm vs. 94–184 × 13–15 µm). In the original description by Ellis (1958), *S. tropicale* was characterized by even longer conidiophores (40–340 µm) and larger conidia (80–230 µm), highlighting the morphological variability. These differences may be attributed to environmental factors such as geography, humidity, temperature, or the developmental stage of the specimens. However, the morphological characteristics of our specimens fall within the range of the features described in the original description by Ellis (1958). Previously, *S. tropicale* has been reported on dead branches of various dicotyledonous plants, including *Averrhoa carambola*, *Blighia unijugata*, *Camellia sinensis*, *Psidium guajava*, *Chrysophyllum albidum*, *Cola nitida*, *Dillenia indica*, *Hevea brasiliensis*, *Glyphaea brevis*, *Homalium aylmeri*, *Lecaniodiscus cupanioides*, *Ochthocosmus africanus*, *Parinari excelsa*, *Phyllanthus discoideus*, and *Pimenta officinalis*. In this study, we report *S. tropicale* on a new host monocot plant, *Pinus yunnanensis*. The strain GMB5105 is therefore designated as a new host record.

Discussion

Analysis and discussion of *Sporidesmium tropicale* in Clade C

In our phylogenetic analysis (Fig. 1), Clade C encompasses *Sporidesmium tropicale* (GMB5105, GMB5109), *S. tropicale* (DLUCC 1689), *S. tropicale* (MFLUCC 17–0344), and *S. tropicale* (MFLU 17C0850). It forms an independent branch distinct from Clade A (*Sporidesmium*) and Clade B (*Ellisembia*) with high support values (ML/BI = 94/0.99). Morphologically, the conidiophores of *S. tropi-*

cale are relatively similar to those of *Sporidesmium* species. However, there are notable differences in their conidia. The conidia of *S. tropicale* are pyriform, rostrate, and obclavate, with a long and slender apex. They are straight or slightly curved, tapering toward the apex. Their color is dark brown, with a paler brown apex that is 2–3 µm wide; they possess 4–17 septa. In contrast, the conidia of *sporidesmium*-like species (Clade A) are obclavate or cylindrical with tapering ends, a hyaline apex, and a color ranging from pale brown to brown. Additionally, the conidiogenous cells of *S. tropicale* are holoblastic, whereas those of *sporidesmium*-like species (Clade A) are percurrent (Table 2) (Zhang et al. 2017; Yang et al. 2018; Bao et al. 2021; Senwanna et al. 2021).

Based on the morphological differences between *S. tropicale* and *Sporidesmium* species, this study suggests that *S. tropicale* may be classified as a distinct genus. However, to date, no similar species have been reported. Consequently, the criteria for establishing it as a separate genus have not been met, and the original species name is retained in this study.

Morphological discussion and analysis of the three species in Clade D

In our phylogenetic analysis (Fig. 1), Clade D encompasses *Ellisembia yuxiense* (GMB5104, GMB5108), *Ellisembia calyptrata* (HKUCC 10821), and *Ellisembia cryptomeriae* (UESTCC 23 0227). It forms an independent branch distinct from Clade A, Clade B, and Clade C (Sporidesmiaceae) with high statistical values (ML/BI = 99/1). Morphologically, notable size disparities are observed in both conidiophores and among *E. yuxiense* (GMB5104, GMB5108), *E. calyptrata* (HKUCC 10821), and *E. cryptomeriae* (UESTCC 23 0227) (Wu and Zhuang 2005; Tian et al. 2024). Furthermore, the conidiogenous cells of *E. yuxiense* (GMB5104, GMB5108) exhibit similarities to those of the type species of *Ellisembia*: *Ellisembia coronata* (CCF 6699). However, the differences between these two species are primarily manifested in the variations in size and color of their conidiophores and conidia (Table 2).

Discovery of new fungal species and host records enriches understanding of Sporidesmiaceae diversity and ecology in Yunnan Province, China

The discovery of two new fungal species (*E. yuxiense* and *S. ailaoshanense*) and a new host record (*S. tropicale* on *Pinus yunnanensis*) enhances our understanding of fungal diversity in Yunnan, China. Integrating morphological and molecular data is crucial for accurate classification in Sporidesmiaceae. Phylogenetic analyses support these new taxa and clarify their relationships. Morphological differences align with molecular divergences, highlighting ecological adaptability and evolutionary divergence. The new host record expands *S. tropicale*'s ecological range, suggesting host-specific adaptations. Further studies are needed to investigate their ecological roles and distribution patterns (Hyde et al. 2020; Bao et al. 2021).

Conclusion

Our study highlights the distinct evolutionary positions of *Sporidesmium tropicale* in Clade B and *Ellisembia* species in Clade C within Sporidesmiaceae, supported by high phylogenetic support values. Morphological disparities, par-

ticularly in conidial characteristics and conidiogenous cell types, underscore potential taxonomic distinctions.

However, there is currently insufficient evidence to warrant the establishment of new genera. The discovery of new species and a host record enhances our understanding of fungal diversity in Yunnan, emphasizing the need for integrated morphological and molecular approaches in future taxonomic and ecological research.

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Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

Use of AI

No use of AI was reported.

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Conceptualization: Qinfang Zhang, Qirui Li, and Lili Liu. Collection and morphological examinations: Qinfang Zhang, Changtao Lu, and Yulin Ren. Molecular sequencing and phylogenetic analyses: Qinfang Zhang, Kamran Habib, Lili Liu. Specimen identification: Nalin N. Wijayawardene, Chuangen Lin, and Qirui Li. Original draft preparation: Qinfang Zhang, Qirui Li. Review and editing and supervision: Hind A. Al-Shwaiman, Abdallah M. Elgorban, Chuangen Lin, Xiangchun Shen, Jichan Kang, Nalin N. Wijayawardene, and Qirui Li. All authors have read and agreed to the published version of the manuscript.

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Data availability

All specimens are deposited in the herbaria of Guizhou Medical University (GMBH) and the Kunming Institute of Botany, Chinese Academy of Sciences (KUN-HKAS). Sequences have been deposited in GenBank. The alignment file can be obtained from the corresponding author upon request.

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